3D SEGMENTATION OF GLIOMA FROM BRAIN MR IMAGES USING SEEDED REGION GROWING AND FUZZY C-MEANS CLUSTERING

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Abstract

This paper reports 3-D segmentation of glioma from brain MR images. We discuss two algorithms for brain MR image segmentation. The images used are axial MR images of the human brain. The images show a glioma. The objective is to segment the tumor and edema surrounding it from the images. Initially the images are pre-processed by contrast adjustment. Segmentation is performed by two algorithms: seeded region growing and fuzzy c-means clustering. After the images are segmented, the volumes of the segmented regions are measured. The segmentation has been performed in MATLAB. Finally the results are rendered in 3D in AMIRA.

Keywords—*MRI, glioma, contrast adjustment, seeded region growing, fuzzy c-means clustering*

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1. INTRODUCTION

Brain image segmentation is the process of separating diseased brain tissue from normal tissue [1]. In brain MRI analysis, image segmentation is commonly used for measuring and visualizing the brain's anatomical structure. Segmentation of sub-cortical features from brain images is important for detecting abnormal brain patterns [2].

The primary objective of this work is the segmentation of brain MR images. The tumor under consideration is a glioma. The tumor and edema surrounding it have been segmented out. Two segmentation algorithms have been used: seeded region growing and fuzzy c-means (FCM) clustering. The results are rendered in 3D using AMIRA^{TM} software and volume measurements are made for the segmented regions.

2. GLIOMA

A tumor is a tissue that grows abnormally due to uncontrolled cell division. Normally cell growth occurs in a controlled manner. A tumor is also called a lesion or neoplasm. Brain tumors are broadly classified into two types [3]: primary and secondary. Primary brain tumors originate in the brain. Secondary brain tumors originate in other parts of the body and spread to the brain.

Gliomas are primary brain tumors; they originate from glial cells in the brain.

3. IMAGE SEGMENTATION

Image segmentation is the process of partitioning an image into mutually exclusive regions such that each region is spatially contiguous and pixels within a region are homogeneous with respect to a pre-defined criterion [4].

Medical image segmentation is usually done manually by trained experts [5]. Manual segmentation is too cumbersome and time consuming. It has also been observed that manual segmentation is subject to operator bias [6]. Automated segmentation can be used as a first step before further manual segmentation [7], if required. By incorporating manual and automated segmentation, we can develop segmentation techniques which are faster and reliable [8].

4. DATA

The data set consists of 192 axial brain MR images. They are grayscale images of resolution 512 x 512. They show a glioma. Each slice has a thickness of 6 mm. The Fields of View along x axis and y axis are 125 mm and 152 mm respectively.

Image segmentation was performed on MATLAB platform. 3-D rendering was obtained in AMIRA^{TM}.

5. CONTRAST ADJUSTMENT

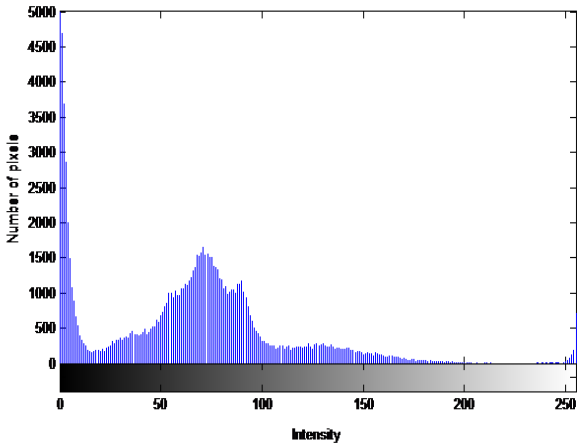
The images obtained are Grayscale; their pixel intensities range from 0 to 255. The tumor and edema pixels lie within [124, 187] and [46, 64] respectively. Contrast adjustment improves the contrast of tumor and edema regions with respect to their backgrounds. After contrast adjustment, the pixel intensities of tumor and edema become [170, 255] and [0, 21] respectively.

Table 1

Tumor pixels	Minimum intensity	Maximum intensity
Original image	124	187
Contrast adjusted image	170	255

Table 2

Edema pixels	Minimum intensity	Maximum intensity
Original image	46	64
Contrast adjusted image	0	21



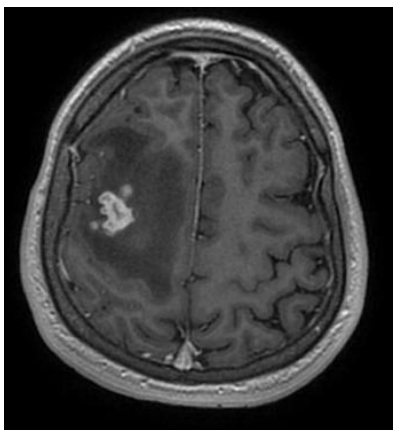
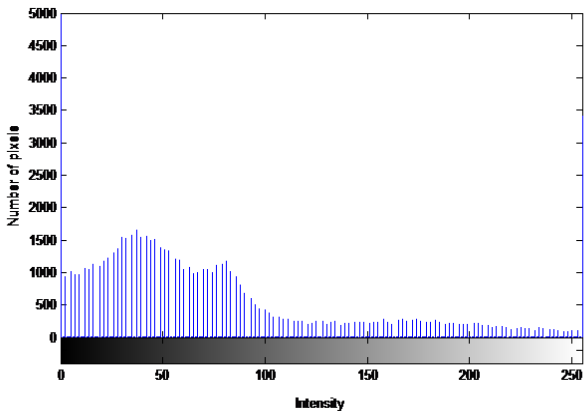


Fig. 1 (a) Sample image & histogram



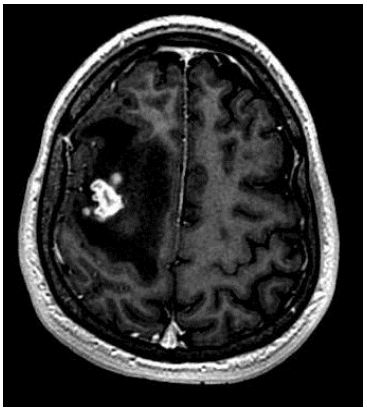


Fig. 1(b) Image & histogram after contrast adjustment

6. REGION GROWING

6.1 Introduction

The algorithm starts from a point within the region and grows outwards until it reaches the boundaries of the region [9]. Seeded region growing has been used in the segmentation of MR images acquired in all three orientations [10].

6.2 Seed Selection

The point from which region growing process starts is the seed point. If no a priori information is available, the seed may have to be selected automatically [11]. This can be done using the histogram. The pixels which correspond to the strongest peaks on the histogram can be chosen as the seeds [12]. To start the process of region growing, any pixel that lies within the required region is selected as the seed. There is a chance that the selected seed point may fall on a pixel that is not characteristic of the region. To solve this, multiple seeds are selected and the average of their intensities is computed. Any of the points that lie within a certain range of the average is chosen as the seed point.

6.3 Neighborhood Selection

A morphological structural element is used to perform a dilation operation on the image. This gives a new structure which consists of the original structure and its immediate neighboring pixels. From this new structure, the original structure is removed leaving only the neighboring pixels. Thus the neighboring pixels alone are selected.

6.4 Homogeneity Criterion

The set of neighboring pixels is tested for the homogeneity criterion which may be based on the intensity or any other feature of the image [13]. If intensity is used, the average intensity of the current region is calculated. For each neighboring pixel, the difference in intensity with the average of the current region is calculated. If this difference is less than a certain threshold, that pixel is to be included in the region. If it is higher than the threshold, it is to be excluded.

6.5 Termination Of Region Growing

The neighborhood selection and homogeneity testing are performed iteratively. In any step of the iteration, if none of the neighboring pixels satisfy the homogeneity criterion, then the region does not grow in that step. It means that none of the neighboring pixels are similar to the growing region, i.e. the region boundary has been reached. When this happens, the region growing process is terminated.

6.6 Results

In the original MR images, the tumor lies between the pixel intensities [124, 187] and edema lies between [46, 64]. After contrast adjustment, the tumor lies between [170, 255] and edema lies between [0, 21]. Homogeneity criterion is defined as pixel intensity lying within ±25 of the seed pixel intensity. As the segmentation is being done in 3-D, a 3-D structuring element which selects the 26-connected neighborhood is used.

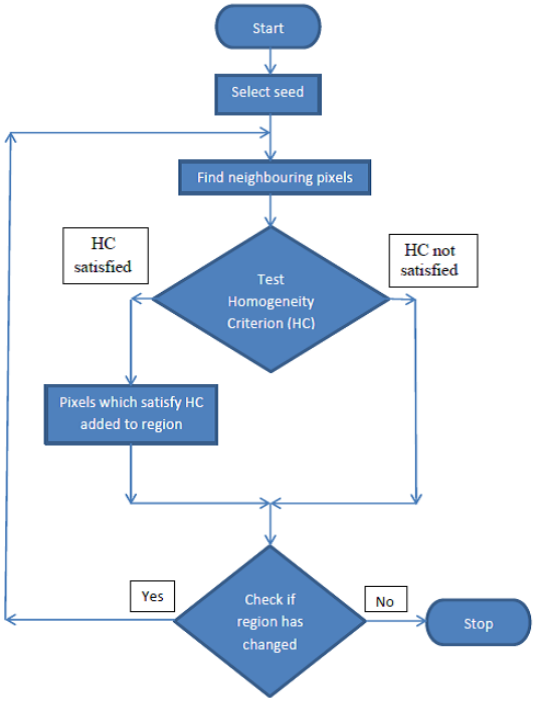


Fig. 2.1 Flowchart of seeded region growing

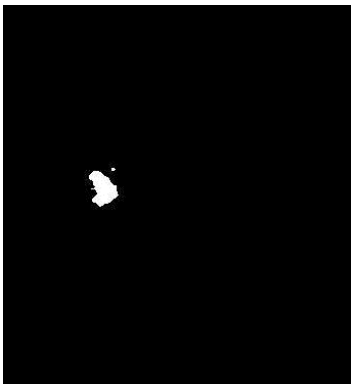


Fig. 2.2 (a) Sample from segmented tumor set

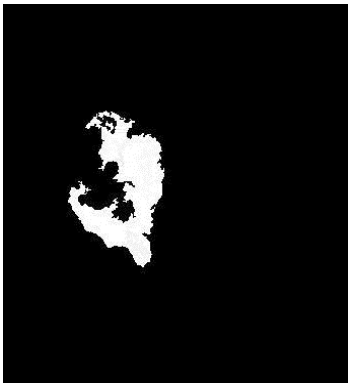


Fig. 2.2 (b) Sample from segmented edema set

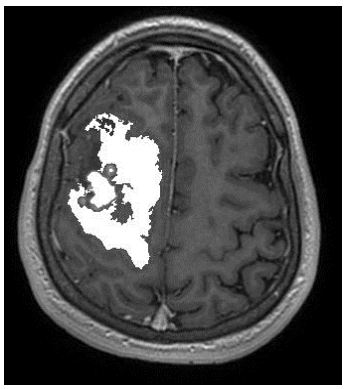


Fig. 2.2(c) Tumor and edema superimposed on original data

7. FUZZY C-MEANS CLUSTERING

7.1 Introduction

Clustering is a method of dividing a data set into different groups or clusters. The data points are assigned to clusters and each cluster can be characterized by a single reference point. This reference point is generally an average of the points in the cluster. In c-means clustering, 'c' reference points are selected.

Usually when a data set is divided into clusters, each data point is assigned definitively to any one of the clusters. This is called hard clustering. In fuzzy clustering, each data point is assigned a membership function to each cluster [14]. The membership function of a data point to a cluster indicates the degree to which the data point belongs to that cluster [15]. The membership functions are represented in the form of a matrix called fuzzy partition matrix. The fuzzy membership function is constrained to have values between 0 and 1 [16].

7.2 Algorithm

Fuzzy c-means clustering is based on the optimization of a c-means objective function. The functional which is to be optimized is given as:

$$\sum_{i=1}^{n} \sum_{j=1}^{c} w_{ij}^{m} ||x_i - c_j||^2$$

where: $X = \{x_1, x_2 \ldots, x_n\}$ is the set of data points
$C = \{c_1, c_2 \ldots, c_c\}$ is the set of cluster centers
$W = w_{i,j} \in [0,1]$, i=1,2 …, n, j=1,2 …,c

Fuzzy clustering is done by iterative optimization of the above function with the update of membership $u_{i,j}$ and cluster centers c_j by:

$$u_{i,j} = \frac{1}{\sum_{k=1}^{c}\left[\frac{||x_i - c_j||}{||x_i - c_k||}\right]^{\frac{2}{m-1}}} \quad (1)$$

7.3 Results

When FCM is applied for brain tumor segmentation, the first step is to define a set of tissue classes. Each pixel is then assigned membership values to the tissue classes. The fuzzy membership functions, constrained to lie between 0 and 1, indicate the similarity of the pixel to each of the tissue classes. Then the pixels are given different intensity values in the segmented result.

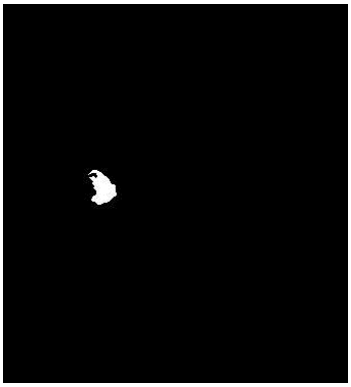


Fig. 3(a) Sample from segmented tumor set

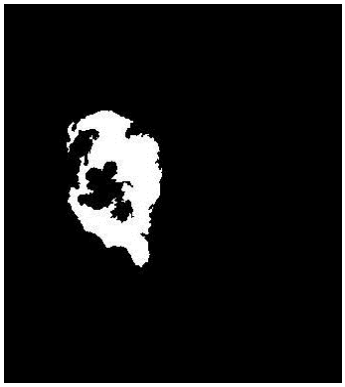


Fig. 3(b) Sample from segmented edema set

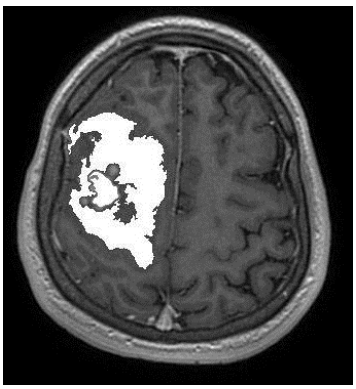


Fig. 3(c) Tumor and edema superimposed on original data

8. VOLUME MEASUREMENTS

The volume of a voxel is calculated as:

$$Volume = \frac{FOV_x}{N_x} \times \frac{FOV_y}{N_y} \times S.T$$

where FOV_x and FOV_y are the fields of view along x and y axes respectively. S.T is the slice thickness.

FOV_x is 125 mm, FOV_y is 152 mm and slice thickness is 6 mm. Substituting these values in the equation gives the volume of a voxel as 0.43488 mm^3.

From each of the segmented results, the number of voxels which represent the tumor and the edema are counted. The volume of the tumor/edema is found by multiplying the number of voxels with the volume of a voxel. These values are given in the following tables.

Table 3

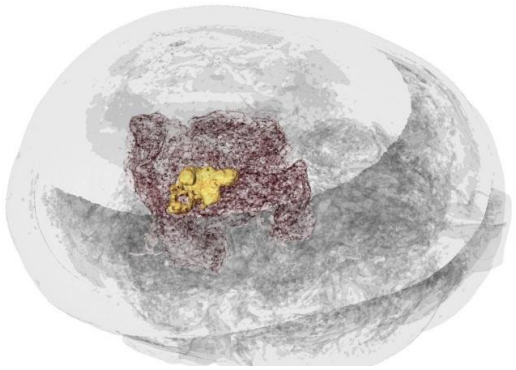
Region growing	**Tumor**	**Edema**
Number of voxels	9818	189070
Volume (mm^3)	4269.65	82222.76

Table 4

FCM	**Tumor**	**Edema**
Number of voxels	9963	214888
Volume (mm^3)	4432.71	93450.49

9. THREE-DIMENSIONAL RENDERING

3-D rendering of the brain tumor and edema was obtained using AMIRA software. The tumor region is shown in yellow color and the edema surrounding it is in dark red color. The original data set is set to be transparent so that tumor and edema are visible. These 3D views are shown in the following figures.



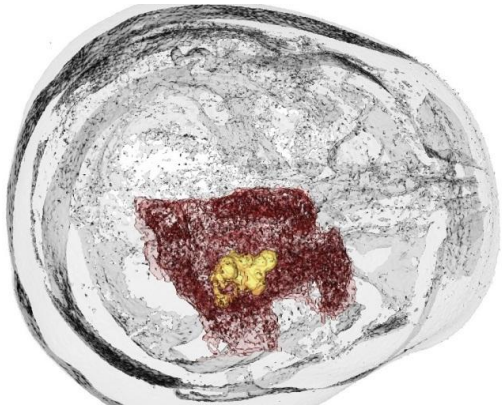


Fig. 4 Three-D rendering of tumor and edema superimposed on original data set

10. CONCLUSION

Both the techniques used for segmentation are semi-automatic. The segmentation results and the volume measurements made can help in pre-surgical assessment of the tumor. For proper validation of the results, they need to be compared with manual segmentation results for the same data. These algorithms are both quite fast; they take only a few minutes to perform the segmentation, whereas manual segmentation may be rather time-consuming.

Although these results are promising, further research is required in this field. One main concern the clinical fraternity has with automated segmentation algorithms is that there is no clear standardization procedure for automated segmentation techniques. Also with these methods, there is a lack of interpretability as compared to segmentation done by trained experts [17].

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